OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: November 7, 2003, 16:02:58 ; Search time 28 Seconds
(without alignments)
3412.068 Million cell updates/sec

Title: US-09-704-272-2
Perfect score: 11785
Sequence: 1 MACWPQLRLLLWKNLTFRRR..............VDVAVLTSFLQDEKVKESYV 2258
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:**
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6901	58.6	1375	3	US-08-665-259-26	Sequence 26, Appl
2	6901	58.6	1375	3	US-08-762-500-26	Sequence 26, Appl
3	3112.5	26.4	1457	3	US-08-665-259-27	Sequence 27, Appl
4	3112.5	26.4	1457	3	US-08-762-500-27	Sequence 27, Appl
5	2618	22.2	1684	3	US-08-665-259-25	Sequence 25, Appl
6	2618	22.2	1684	3	US-08-762-500-25	Sequence 25, Appl
7	2618	22.2	1704	3	US-08-762-500-75	Sequence 75, Appl
8	359	3.0	315	4	US-09-328-352-4388	Sequence 4388, Appl
9	355	3.0	322	4	US-09-328-352-4662	Sequence 4662, Appl
10	353	3.0	332	4	US-09-107-532A-3752	Sequence 3752, Ap
11	352.5	3.0	335	4	US-09-252-991A-20837	Sequence 20837, Ap
12	344	2.9	589	4	US-09-328-352-7592	Sequence 7592, Ap
13	338.5	2.9	1280	2	US-09-583-276-19	Sequence 19, Appl
14	338	2.9	402	4	US-09-107-532A-5360	Sequence 5360, Ap
15	337.5	2.9	1280	5	US-09-767-594-2	Sequence 2, Appli
16	337.5	2.9	1280	6	Patent No. 5206352-4205	Patent No. 5206352
17	335.5	2.8	291	2	US-08-784-649A-4205	Sequence 4205, Appl
18	335	2.8	1279	2	US-08-752-447-2	Sequence 2, Appli
19	335	2.8	291	2	US-09-316-167-2	Sequence 2, Appli
20	326.5	2.8	1280	4	US-09-252-991A-22946	Sequence 22946, A
21	326.5	2.8	1280	4	US-09-252-991A-28171	Sequence 28171, A
22	323	2.7	929	4	US-09-252-991A-18351	Sequence 18351, A
23	322.5	2.7	788	4	US-09-107-532A-4983	Sequence 4983, Ap
24	319.5	2.7	607	4	US-09-252-991A-13351	Sequence 13351, A
25	318	2.7	254	4	US-09-134-001C-3570	Sequence 3570, Ap
26	317	2.7	406	4	US-09-252-991A-21204	Sequence 21204, Ap
27	316.5	2.7	309	4	US-09-252-991A-20275	Sequence 20275, A
28	316.5	2.7	460	4	US-09-134-001C-3369	Sequence 3369, Ap
29	316	2.7	319	4	US-09-634-238-243	Sequence 243, App
30	310.5	2.7	1275	3	US-09-120-513-2	Sequence 2, Appli
31	310.5	2.6	1275	3	US-09-450-105-2	Sequence 2, Appli
32	310	2.6	1302	1	US-08-232-537-2	Sequence 2, Appli
33	302	2.6	329	4	US-09-107-532A-4844	Sequence 4844, Ap
34	299	2.5	350	4	US-09-107-532A-6978	Sequence 6978, Ap
35	299	2.5	528	4	US-09-107-532A-6340	Sequence 6340, Ap
36	296.5	2.5	304	4	US-09-107-532A-5424	Sequence 5424, Ap
37	293	2.5	337	4	US-09-107-532A-5550	Sequence 5550, Ap
38	287.5	2.4	1408	1	US-08-612-521-2	Sequence 2, Appli
39	287	2.4	1349	2	US-08-612-734B-2	Sequence 2, Appli
40	285.5	2.4	233	4	US-09-627-376-12	Sequence 12, Appl
41	284	2.4	231	4	US-09-134-001C-3824	Sequence 3824, Ap
42	281.5	2.4	288	4	US-09-107-532A-7040	Sequence 7040, Ap
43	280.5	2.4	307	4	US-09-134-001C-3539	Sequence 3539, Ap
44	276	2.3	257	4	US-09-107-532A-5192	Sequence 5192, Ap
45	276	2.3	303	4	US-09-252-991A-20275	Sequence 20275, A

ALIGNMENTS

RESULT 1
US-08-665-259-26
Sequence 26, Application US/08665259
Patent No. 6028173

GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy C.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusets
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG5-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-665-259-26

Query Match   58.6%; Score 6901; DB 3; Length 1375;
Best Local Similarity 96.9%;
Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

```
OM protein - protein search, using sw model

                                     GenCore version 5.1.6
                                     Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:          November 7, 2003, 16:01:07 ; Search time 25 Seconds
                                              (without alignments)
                                              4247.452 Million cell updates/sec

Title:
Perfect score:   11785
Sequence:        1 MACWPQLRLLLWKNLTFRRR........VDVAVLTSFLQDEKVKESYV 2258

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:   127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_41:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.
```

SUMMARIES   *Date*   *"CERP"*

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11718.5	99.4	2261	2261	1	ABC1_HUMAN	O95477 homo sapien
2	11203.5	95.1	2261	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5836	49.5	2273	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4217	35.8	2436	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	4073	34.6	2434	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2618	22.2	1704	1704	1	ABC3_HUMAN	Q9758 homo sapien
7	1523	12.9	1704	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.5	330	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.2	343	343	1	NODI_RHISN	P55476 rhizobium s
10	366	3.1	304	304	1	NODI_RHIS3	P72335 rhizobium s
11	347	2.9	308	308	1	YADG_ECOLI	P36879 escherichia
12	347	2.9	335	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	345	2.9	340	340	1	NODI_RHILO	P23703 rhizobium l
14	343.5	2.9	347	347	1	NODI_RHIGA	P50332 rhizobium g
15	337.5	2.9	1280	1280	1	MDR1_HUMAN	P08183 homo sapien
16	336	2.9	894	894	1	YHIH_ECOLI	P37624 escherichia
17	331.5	2.8	355	355	1	NDI1_RHIME	O52618 rhizobium m
18	329.5	2.8	578	578	1	YBHF_ECOLI	P75776 escherichia
19	327.5	2.8	308	308	1	NOSF_PSEST	P19844 pseudomonas
20	327.5	2.8	1281	1281	1	MDR3_CRIGR	P23174 cricetulus
21	324.5	2.8	306	306	1	NODI_BRAJA	P26050 bradyrhizob
22	324.5	2.8	1276	1276	1	MDR2_MOUSE	P21440 mus musculu
23	323	2.8	347	347	1	NODI_CRIGR	P21448 cricetulus
24	321.5	2.7	1276	1276	1	PMD1_SCHPO	P36619 schizosacch
25	320	2.7	1362	1362	1	MDR2_MOUSE	P21447 mus musculu
26	317.5	2.7	1276	1276	1	MDR2_CRIGR	P21449 cricetulus
27	315.5	2.7	311	311	1	NODI_RHILV	P08720 rhizobium 1
28	313	2.7	354	354	1	Y415_SYNY3	P22040 synechocyst
29	313	2.7	1277	1277	1	MDR1_RAT	P43245 rattus norv
30	313	2.7	1278	1278	1	MDR2_RAT	Q08201 rattus norv
31	309	2.6	1276	1276	1	MDR1_MOUSE	P06795 mus musculu
32	305	2.6	305	305	1	NODI_BRASS	Q9z313 bradyrhizob
33	304.5	2.6	1294	1294	1	YOH5_YEAST	Q08234 saccharomyc
34	301	2.6	381	381	1	OPBA_BACSU	Q45460 bacillus su
35	299	2.5	380	380	1	OPCA_BACSU	O34992 bacillus su
36	296	2.5	335	335	1	Y719_ANASP	Q05067 anabaena sp
37	292.5	2.5	262	262	1	YA23_METJA	Q58429 methanococc
38	292.5	2.5	305	305	1	YHCH_BACSU	P54592 bacillus su
39	290.5	2.5	274	274	1	Y179_MYCPN	Q50294 mycoplasma
40	288	2.4	1321	1321	1	AB11_HUMAN	O95342 homo sapien
41	287.5	2.4	274	274	1	Y179_MYCGE	Q47425 mycoplasma
42	287.5	2.4	1279	1279	1	MDR3_HUMAN	P21439 homo sapien
43	284.5	2.4	1321	1321	1	MDR1_CAEEL	P34712 caenorhabdi
44	284	2.4	306	306	1	BCRA_BACLI	P42232 bacillus li
45	282.5	2.4	1336	1336	1	MAM1_SCHPO	P78966 schizosacch

RESULT 1
ABC1_HUMAN

ALIGNMENTS

```
ID   ABC1_HUMAN     STANDARD;      PRT;    2261 AA.
AC   O95477; Q96S56; Q96T85; Q9NQV4; Q9NU06; Q9UN07; Q9UN08; Q9UN09;
AC   Q9NU05;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE   transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux
DE   regulatory protein).
GN   ABCA1 OR ABC1 OR CERP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20345099; PubMed=10884428;
RA   Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA   Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA   Haudenschild C.C., Prades C., Chimini G., Blackmon E.B.,
RA   Francois T.L., Duverger N., Rubin E.M., Rosier M., Denefle P.,
RA   Fredrickson D.S., Brewer H.B. Jr.;
RT   "Complete genomic sequence of the human ABCA1 gene; analysis of the
RT   human and mouse ATP-binding cassette A promoter.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Schwartz K., Lawn R.M., Wade D.P.;
RT   "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
RT   regulated by LXR.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21251004; PubMed=11352567;
RA   Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT   "Human and mouse ABCA1 comparative sequencing and transgenesis
RT   studies revealing novel regulatory sequences.";
RL   Genomics 73:66-76(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,
RA   Kioka N., Amachi T., Yokoyama S., Ueda K.;
RT   "A new topological model of functional human ABCA1-signal peptide
RT   cleavage and glycosylation of a large extracellular domain.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 21-2261 FROM N.A.
RX   MEDLINE=99194549; PubMed=10092505;
RA   Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,
RA   Chimini G., Kaminski W.E., Schmitz G.;
RT   "Molecular cloning of the human ATP-binding cassette transporter 1
RT   (hABC1): evidence for sterol-dependent regulation in macrophages.";
RL   Biochem. Biophys. Res. Commun. 257:29-33(1999).
RN   [6]
```

OM protein - protein search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.6

Run on: November 7, 2003, 16:02:12 ; Search time 35 Seconds
(without alignments)
6204.254 Million cell updates/sec

Title: US-09-704-272-2
Perfect score: 11785
Sequence: 1 MACWPQLRLLLWKNLTFRRR..........VDVAVLTSFLQDEKVKESYV 2258

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR 76:*
        1:      pir1:*
        2:      pir2:*
        3:      pir3:*
        4:      pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10869.5	92.2	2201	2	A54774	ATP binding casset
2	3332.5	28.3	1529	2	A59189	ATP-binding casset
3	3112.5	26.4	1472	2	B54774	ATP binding casset
4	2621	22.2	1704	2	S71363	probable ATP-bindi
5	2618	22.2	1704	2	A54188	ATP-binding casset
6	2043	17.3	1802	2	T33783	hypothetical prote
7	1985.5	16.8	1816	2	A84845	probable ABC trans
8	1858	15.1	1447	2	T12600	hypothetical prote
9	1778.5	15.1	1317	2	C88925	probable ABC trans
10	1530	13.0	1758	2	F83559	protein C48B4.4b [
11	1523	12.9	1704	2	F88559	protein F33E11.4 [
12	1520.5	12.9	1767	2	T42749	ATP-binding casset
13	1398	11.9	1246	2	S60124	transport protein
14	1153	9.8	1564	2	T21121	hypothetical prote
15	1017	8.6	1431	2	T22748	hypothetical prote
16	1013.5	8.6	373	2	T41150	hypothetical prote
17	846	7.2	269	2	T46467	hypothetical prote
18	784	6.7	1011	2	T07712	hypothetical prote
19	684.5	5.8	900	2	T07717	probable ABC-type
20	662	5.6	895	2	T07714	probable ABC-type
21	649	5.5	722	2	T07716	probable ABC-type
22	638.5	5.4	925	2	T07713	probable ABC-type
23	619	5.3	1336	2	T18288	ABC transport prot
24	485	4.1	196	2	T12512	hypothetical prote
25	432	3.7	339	2	S74048	probable daunorubi
26	426.5	3.6	324	2	C71081	probable daunorubi
27	422.5	3.6	664	2	T07715	probable ABC-type
28	419.5	3.6	328	2	E75108	daunorubicin resis
29	412.5	3.5	310	2	C96929	ABC-type multidrug
30	411	3.5	330	2	S27707	daunorubicin resis
31	410.5	3.5	327	2	D72257	hypothetical prote
32	410	3.5	314	2	D97318	ABC-type MDR trans
33	409.5	3.5	398	2	C69485	daunorubicin resis
34	404.5	3.4	297	2	AE1816	ABC transporter (A
35	399.5	3.4	333	2	D72492	probable ABC trans
36	399.5	3.4	310	2	E96920	ABC transporter (A
37	395.5	3.4	311	2	G69803	ABC transporter (A
38	395	3.4	246	2	S75436	hypothetical prote
39	394	3.3	301	2	E72384	ABC transporter, A
40	390	3.3	301	2	D70984	probable MDR prot
41	388	3.3	259	2	H97301	ABC-type MDR trans
42	387	3.3	331	2	S73019	daunorubicin resis
43	386	3.3	350	2	B69065	ABC transporter (A
44	385	3.2	312	2	H97342	ABC-type MDR trans
45	378	3.2	130	2	I38906	ATP-binding casset

ALIGNMENTS

RESULT 1
A54774
ATP binding cassette transporter ABC1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Apr-1995 #sequence_revision 05-Apr-1995 #text_change 02-Feb-2001
C;Accession: A54774
R;Luciani, M.F.; Denizot, F.; Savary, S.; Mattei, M.G.; Chimini, G.
Genomics 21, 150-159, 1994
A;Title: Cloning of two novel ABC transporters mapping on human chromosome 9.
A;Reference number: A54774; MUID:94375008; PMID:8088782
A;Accession: A54774
A;Molecule type: mRNA
A;Residues: 1-2201 <LUC>
A;Cross-references: GB:X75926; NID:g495256; PIDN:CAA53530.1; PID:g495257
A;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolo
C;Superfamily: ATP; duplication; nucleotide binding; P-loop
C;Keywords: ATP-binding cassette homology <ABC1>
F;856-1047/Domain: ATP-binding cassette homology <ABC1>
F;873-880/Region: nucleotide-binding motif A (P-loop)
F;1869-2060/Domain: ATP-binding cassette homology <ABC2>
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match   92.2%; Score 10869.5; DB 2; Length 2201;
Best Local Similarity   94.7%; Pred. No. 0;
Matches 2084; Conservative 54; Mismatches 60; Indels 3; Gaps 1;

```
Qy    61 MPSAGTLPWQGIICNANNCFRYPTPGEAPGVVGNENKSIVARLFSDARLLLYSQKDT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     1 MPSAGTLPWQGIICNANNCFRYPTPGEAPGVVGNENKSIVSRLFSDAQRLLLYSQRDT  60

Qy   121 SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH 180
            || || |||| |||| || ||||||||||||||||||| |||||| |||    | |  |
Db    61 SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSLPRSTVDSLLQXNVGLQ 120

Qy   181 KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCCGLPREKLAAAERVLRSNMDILKPIL 240
            |||||||||| ||||||| ||| |||||| || ||| || ||  ||||||  ||||||  
Db   121 KVFLQGYQLHIASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRYNMDILKPVV 180

Qy   241 RTLNSTSPPSKELAEATKTLLHSLGTLAQELFSMRSWSDVRQEVMFLTNVNSSSSSTQI 300
             ||||||  | ||||||| ||| ||| |||||| ||||| |||||||||||||||||||
Db   181 TKLNSTSHLPTQHLAEATTVLLDSLGGLAQELFSTKSWSDMRQEVMFLTNVNSSSSSTQI 240

Qy   301 YQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNDLMK 360
            |||||||||  |||||||||||||||||||||||||| |||| | |||||||||||||||
Db   241 YQAVSRIVCCHPEGGGLKIKSLNWYEDNNYKALFGGNNTEEDVDTFYDNSTTPYCNDLMK 300

Qy   361 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELS 420
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   301 NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVWAEVNKTFQELAVFHDLEGMWEELS 360

Qy   421 PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGS 480
            | |||||||||||||||  ||||| ||  ||| ||||||| |  |||| |  ||| ||||
Db   361 PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQXLDGLDWTAQDIMAFLAKNPEDVQSPNGS 420
```

OM protein - protein search, using sw model

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.6

Run on: November 7, 2003, 16:04:18 ; Search time 48 Seconds
(without alignments)
8079.373 Million cell updates/sec

Title: US-09-704-272-2
Perfect score: 11785
Sequence: 1 MACWPQLRLLWKNLTFRRR.............VDVAVLTSFLQDEKVKESYV 2258

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11734.5	99.6	2261	12	US-10-313-641-9	Sequence 9, Appli
2	11734.5	99.6	2261	12	US-10-313-641-10	Sequence 10, Appl
3	11715.5	99.4	2261	11	US-09-995-542-11	Sequence 11, Appl
4	11715.5	99.4	2261	10	US-09-846-456-11	Sequence 11, Appl
5	11715.5	99.4	2261	2	US-09-984-827-2	Sequence 2, Appl1
6	11714.5	99.4	2261	11	US-09-984-827-129	Sequence 129, App
7	11714.5	99.4	2261	11	US-09-984-827-136	Sequence 136, App
8	11712.5	99.4	2261	11	US-09-984-827-127	Sequence 127, App
9	11712.5	99.4	2261	11	US-09-984-827-128	Sequence 128, App
10	11712.5	99.4	2261	11	US-09-984-827-131	Sequence 131, App
11	11712.5	99.4	2261	11	US-09-984-827-134	Sequence 134, App
12	11712.5	99.4	2261	11	US-09-984-827-135	Sequence 135, App
13	11710.5	99.3	2261	11	US-09-984-827-133	Sequence 133, App
14	11705.5	99.3	2261	11	US-09-984-827-130	Sequence 130, App
15	11704.5	99.3	2261	11	US-09-984-827-132	Sequence 132, App
16	11176.5	94.8	2261	12	US-10-340-097-118	Sequence 118, App
17	11176.5	94.8	2261	12	US-10-336-215-118	Sequence 118, App
18	11176.5	94.8	2261	12	US-10-336-219-118	Sequence 118, App
19	10869.5	92.2	2201	10	US-09-995-542-9	Sequence 9, Appli
20	5838.5	49.5	2310	10	US-09-995-542-10	Sequence 10, Appl
21	5820	49.4	2273	10	US-09-995-542-12	Sequence 12, Appl
22	5799	49.2	2273	12	US-10-340-097-3	Sequence 3, Appli
23	5799	49.2	2273	12	US-10-336-215-3	Sequence 3, Appli
24	5799	49.2	2273	12	US-10-336-219-3	Sequence 3, Appli
25	5716	48.5	2146	12	US-09-995-542-5	Sequence 5, Appli
26	5703	48.4	2144	9	US-09-858-194-2	Sequence 2, Appli
27	5703	48.4	2144	12	US-10-154-419-2	Sequence 2, Appli
28	5702	48.4	2235	12	US-10-340-097-6	Sequence 6, Appli
29	5702	48.4	2235	12	US-10-336-215-6	Sequence 6, Appli
30	5702	48.4	2235	12	US-10-336-219-6	Sequence 6, Appli
31	5680.5	48.2	2167	10	US-09-995-542-6	Sequence 6, Appli
32	5558	47.2	2100	10	US-09-995-542-2	Sequence 2, Appli
33	5530.5	46.9	2121	10	US-09-995-542-3	Sequence 3, Appli
34	4227	35.9	2436	15	US-09-795-693-8	Sequence 8, Appli
35	4227	35.9	2436	15	US-10-156-239-8	Sequence 8, Appli
36	4227	35.9	2436	15	US-10-199-485-8	Sequence 8, Appli
37	4014.5	34.1	2001	14	US-10-072-621-8	Sequence 8, Appli
38	3779.5	32.1	1550	10	US-09-995-542-8	Sequence 8, Appli
39	3235.5	27.5	2595	15	US-10-340-097-119	Sequence 119, App
40	3110.5	26.4	1472	12	US-10-336-215-119	Sequence 119, App
41	3110.5	26.4	1472	12	US-10-340-097-119	Sequence 119, App
42	3110.5	26.4	1472	12	US-10-336-219-119	Sequence 119, App
43	3054	25.9	1472	15	US-10-340-097-120	Sequence 120, App
44	2625	22.3	1704	12	US-10-336-215-120	Sequence 120, App
45	2625	22.3	1704	12	US-10-336-215-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-313-641-9

; Sequence 9, Application US/10313641
; Publication No. US20030162758A1
; GENERAL INFORMATION:
; APPLICANT: Ishida, Brian
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Schwartz, Daniel
; TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)
; FILE REFERENCE: P0235IUS2
; CURRENT APPLICATION NUMBER: US/10/313,641
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 2261
; TYPE: PRT
; ORGANISM: Human
US-10-313-641-9

Query Match   99.6%;
Best Local Similarity   99.6%;
Matches 2253; Conservative   2; Mismatches   3; Indels   3; Gaps   1;

```
Qy     1 MACWPQLRLLWKNLTFRRRQTCQLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MACWPQLRLLWKNLTFRRRQTCQLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKA 60

Qy    61 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARLLLYSQKDT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARLLLYSQKDT 120
```

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: November 7, 2003, 16:01:37 ; Search time 64 Seconds
                 (without alignments)
                 9104.418 Million cell updates/sec

Title: US-09-704-272-2
Perfect score: 11785
Sequence: 1 MACWPQLRLLLWKNLTFRRR..........VDVAVLTSFLQDEKVKESYV 2258

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	DB ID	Description
1	10165	86.3	2260	13	Q8UVV4	q8uvv4 gallus gall
2	7334.5	62.2	1487	11	Q8BPY1	q8bpy1 mus musculu
3	5838.5	49.5	2019	11	O35600	o35600 mus musclu
4	5825	49.4	2281	6	O02698	o02698 bos taurus
5	5723	48.6	2146	4	Q8BZC4	q8bzc4 homo sapien
6	5711	48.5	2146	4	Q9NR73	q9nr73 homo sapien
7	5706	48.4	2146	4	Q8IZY2	q8izy2 homo sapien
8	5681.5	48.2	2159	11	Q91V24	q91v24 mus musculu
9	5323.5	45.2	2008	4	Q9ESR9	q9esr9 ratus norv
10	4232	35.9	2434	11	Q96S58	q96s58 homo sapien
11	4227	35.9	2436	11	Q9HC28	q9hc28 homo sapien
12	3209	27.2	2347	4	Q8IZW6	q8izw6 homo sapien
13	3200	27.2	2277	4	Q96JT3	q96jt3 homo sapien
14	2698.5	22.9	1764	5	Q8MUA3	q8mua3 strongyloce
15	2562.5	21.7	1704	11	Q8R420	q8r420 mus musculu
16	2463	20.9	1713	5	Q9VRG4	q9vrg4 drosophila
17	2146.5	18.2	1846	10	Q8W010	q8w010 arabidopsis
18	2043.5	17.3	1802	5	Q9TXV8	q9txv8 caenorhabdi
19	2024	17.2	1547	5	O01790	o01790 caenorhabdi
20	2019	17.2	1660	5	Q9VVJ9	q9vvj9 drosophila
21	2015.5	17.1	1843	5	Q9GQS2	q9gqs2 leishmania
22	2007.5	17.0	867	4	Q96HC2	q96hc2 homo sapien
23	1984	16.8	1896	5	Q8N898	q8n898 leishmania
24	1918	16.3	1621	5	Q8T6J5	q8t6j5 dictyosteli
25	1828	15.5	1631	5	Q8T6J4	q8t6j4 dictyosteli
26	1819.5	15.4	1662	5	Q8T6J1	q8t6j1 dictyosteli
27	1807	15.3	1608	5	Q8T6J2	q8t6j2 dictyosteli
28	1800	15.3	1750	5	Q8T6J3	q8t6j3 dictyosteli
29	1794.5	15.2	1702	5	Q9BKL1	q9bkl1 dictyosteli
30	1527.5	13.0	1526	5	Q9VVK6	q9vvk6 drosophila
31	1502.5	12.7	1642	4	Q8CF82	q8cf82 rattus norv
32	1469	12.5	1642	4	Q9NY14	q9ny14 homo sapien
33	1467	12.4	1642	4	Q8WW27	q8ww27 homo sapien
34	1443	12.2	1642	4	Q8K448	q8k448 mus musculu
35	1413	12.0	1222	10	Q8S8T6	q8s8t6 arabidopsis
36	1411.5	12.0	1623	4	Q8K449	q8k449 mus musculu
37	1408	11.9	1543	4	Q8WW24	q8ww24 homo sapien
38	1369.5	11.6	1624	4	Q8IUA7	q8iua7 homo sapien
39	1367.5	11.6	1617	4	Q8N139	q8n139 homo sapien
40	1364.5	11.6	1624	4	Q8WW25	q8ww25 homo sapien
41	1358.5	11.5	1617	4	Q8WW26	q8ww26 homo sapien
42	1349.5	11.5	1620	11	Q8K440	q8k440 mus musculu
43	1349.5	11.5	1620	11	Q8K442	q8k442 mus musculu
44	1327.5	11.3	1581	4	O94911	o94911 homo sapien
45	1320	11.2	1624	11	Q8K441	q8k441 mus musculu

ALIGNMENTS

RESULT 1
Q8UVV4

| Q8UVV4 | PRELIMINARY; | PRT; | 2260 AA. |

ID   Q8UVV4   PRELIMINARY;   PRT;   2260 AA.
AC   Q8UVV4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ATP-binding cassette transporter 1.
GN   ABCA1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Attie A.D., Brooks-Wilson A.R., Walker D., McManus B.,
RA   Gray-Kellar M.P., Macdonald M.L.E., Roomp K., Tebon A., Zhang L.-H.,
RA   Mulligan J., Sensen C., Bitgood J.J., Cook M.E., Kastelein J.J.P.,
RA   Hayden M.R.;
RT   "Cholesterol Ester Accumulation in Hepatocytes and Intestinal Lamina
RT   Propria Caused by an ABCA1 Mutation in WHAM Chickens.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF362377; AAL56247.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW   ATP-binding.
SQ   SEQUENCE 2260 AA; 254070 MW; 19D137F342F98662 CRC64;

Query Match 86.3%; Score 10165; DB 13; Length 2260;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 1929; Conservative 163; Mismatches 159; Indels 16; Gaps 8;

Qy 1 MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKA 60

```
OM protein - protein search, using sw model

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:             November 7, 2003, 16:00:12 ; Search time 59 Seconds
                                          (without alignments)
                                          6074.654 Million cell updates/sec

Title:              US-09-704-272-2
Perfect score:      11785
Sequence:           1 MACWPQLRLLIWKNLTFRRR........VDVAVLTSFLQDEKVKESYV 2258

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           1107863 seqs, 15872673 residues

Total number of hits satisfying chosen parameters:    1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          A_Geneseq_19Jun03:*
           1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
           2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
           3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
           4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
           5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
           6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
           7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
           8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
           9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
          10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
          11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
          12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
          13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
          14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
          15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
          16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
          17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
          18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
          19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
          20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
          21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
          22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
          23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
          24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result                  Query
No.     Score   Match   Length  DB      ID          Description
------  ------  ------  ------  --      --          -----------
1       11737.5  99.6    2261   21      AAB38082    Human ABC1 cholest
2       11737.5  99.6    2261   21      AAB38110    Human ABC1 cholest
3       11737.5  99.6    2261   24      ABU11899    Human ATP-binding
4       11734.5  99.6    2261   21      AAB38109    Human ABC1 cholest
5       11734.5  99.6    2261   21      AAB38111    Human ABC1 cholest
6       11734.5  99.6    2261   21      AAB38114    Human ABC1 cholest
7       11734.5  99.6    2261   21      AAB38115    Human ABC1 cholest
8       11734.5  99.6    2261   21      AAB38117    Human ABC1 cholest
9       11733.5  99.6    2261   21      AAB38105    Human ABC1 cholest
10      11733.5  99.6    2261   21      AAB38108    Human ABC1 cholest
11      11732.5  99.6    2261   21      AAB38113    Human ABC1 cholest
12      11732.5  99.6    2261   21      AAB38116    Human ABC1 cholest
13      11731.5  99.5    2261   21      AAB38112    Human ATP binding
14      11730.5  99.5    2261   22      AAB31361    Human ABC1. Homo
15      11730.5  99.5    2261   22      AAB31365    Human ABC1 mutant
16      11726.5  99.5    2261   22      AAB31362    Amino acid sequenc
17      11726.5  99.5    2261   22      AAB31366    Amino acid sequenc
18      11725.5  99.5    2261   21      AAB38104    Human ABC1 cholest
19       11723   99.5    2261   21      AAB38106    Human ABC1 cholest
20      11722.5  99.5    2261   22      AAB31363    Amino acid sequenc
21      11722.5  99.5    2261   21      AAB31367    Amino acid sequenc
22      11715.5  99.4    2259   21      AAB38107    Human ABC1 cholest
23      11715.5  99.4    2261   22      AAE13022    Human ABC1 FHA-3 m
24      11715.5  99.4    2261   22      AAM50228    Human ATP binding
25      11715.5  99.4    2261   22      AAU02176    Human ABC1. Homo
26      11715.5  99.4    2261   22      AAU02177    Human ABC1 mutant
27      11715.5  99.4    2261   23      ABB83111    Human ABC1A transp
28      11715.5  99.4    2261   23      ABP52092    Homo sapiens ABC t
29      11715.5  99.4    2261   23      AAE22000    Human ABC1 full-le
30      11714.5  99.4    2261   23      ABB83117    Polymorphic human
31      11714.5  99.4    2261   23      ABB83124    Polymorphic human
32      11712.5  99.4    2261   22      AAU02183    Human ABC1 mutant
33      11712.5  99.4    2261   23      ABB83115    Polymorphic human
34      11712.5  99.4    2261   23      AAU02188    Human ABC1 mutant
35      11712.5  99.4    2261   23      ABB83116    Polymorphic human
36      11712.5  99.4    2261   23      ABB83119    Polymorphic human
37      11712.5  99.4    2261   23      ABB83122    Polymorphic human
38      11712.5  99.4    2261   23      ABB83123    Polymorphic human
39      11711.5  99.4    2261   22      AAU02189    Human ABC1 mutant
40      11710.5  99.4    2261   23      ABB83121    Polymorphic human
41      11709.5  99.4    2261   22      AAU02181    Human ABC1 mutant
42      11708.5  99.4    2261   22      AAM78550    Human protein SEQ
43      11708.5  99.4    2263   22      ABB11956    Human ABC1 homolo
44      11708.5  99.4    2263   22      AAM79534    Human ABCA1 homolo
45      11707.5  99.3    2261   22      AAU02182    Human protein SEQ
```

ALIGNMENTS

```
RESULT 1
AAB38082

ID   AAB38082 standard; Protein; 2261 AA.
XX
AC   AAB38082;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human ABC1 cholesterol transporter.
XX
KW   Human ABC1 cholesterol transporter; chromosome 9q31;
KW   ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW   Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW   cardiovascular disease; coronary artery disease; coronary restenosis;
KW   cerebrovascular disease; peripheral vascular disease;
KW   Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW   X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW   prognosis; prophylaxis; drug screening; transgenic animal.
XX
OS   Homo sapiens.
XX
PN   WO200005318-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-IB00532.
XX
PR   15-MAR-1999;  99US-0124702.
PR   08-JUN-1999;  99US-0138048.
PR   17-JUN-1999;  99US-0139600.
PR   01-SEP-1999;  99US-0151977.
```